FIG. 1

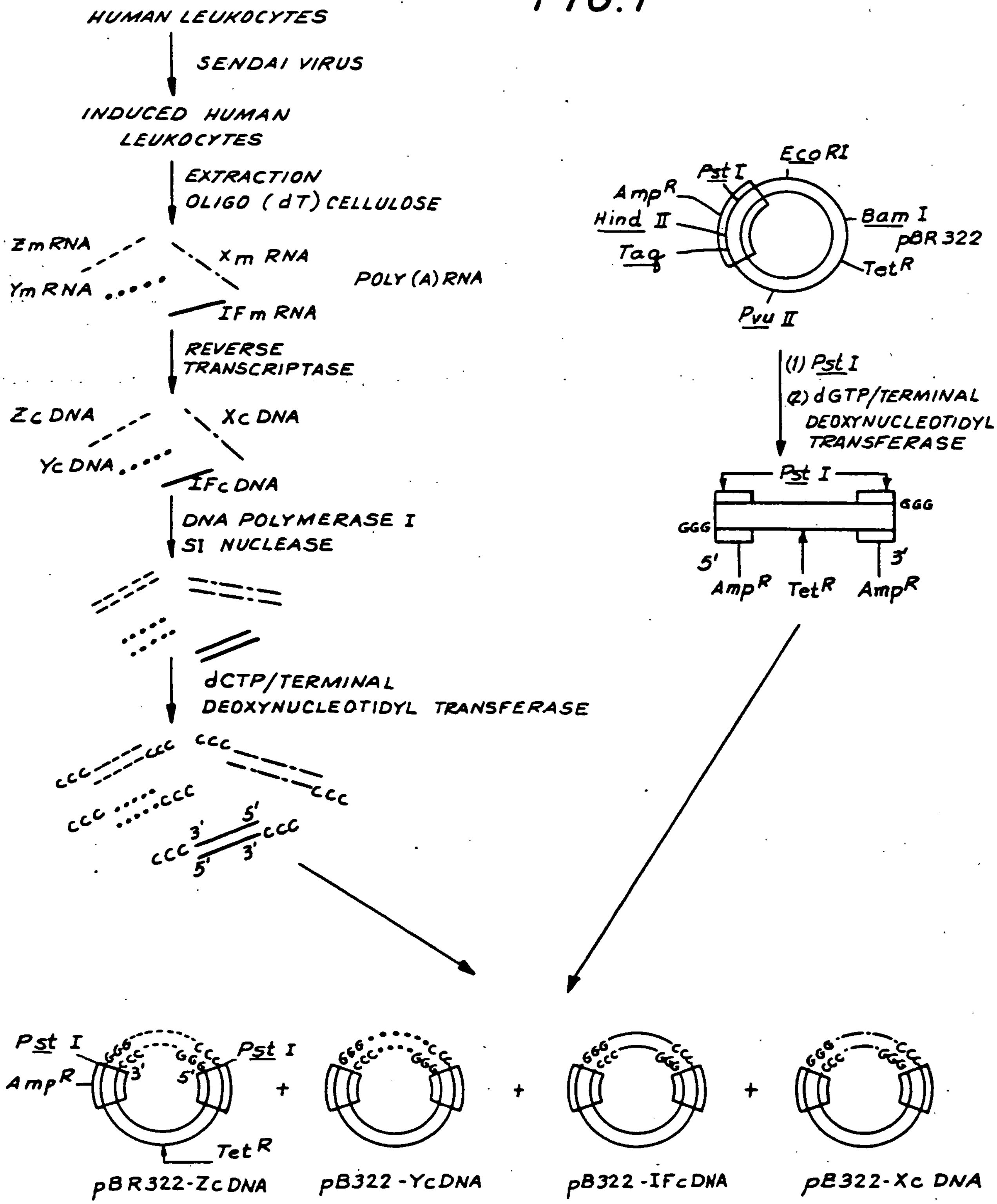
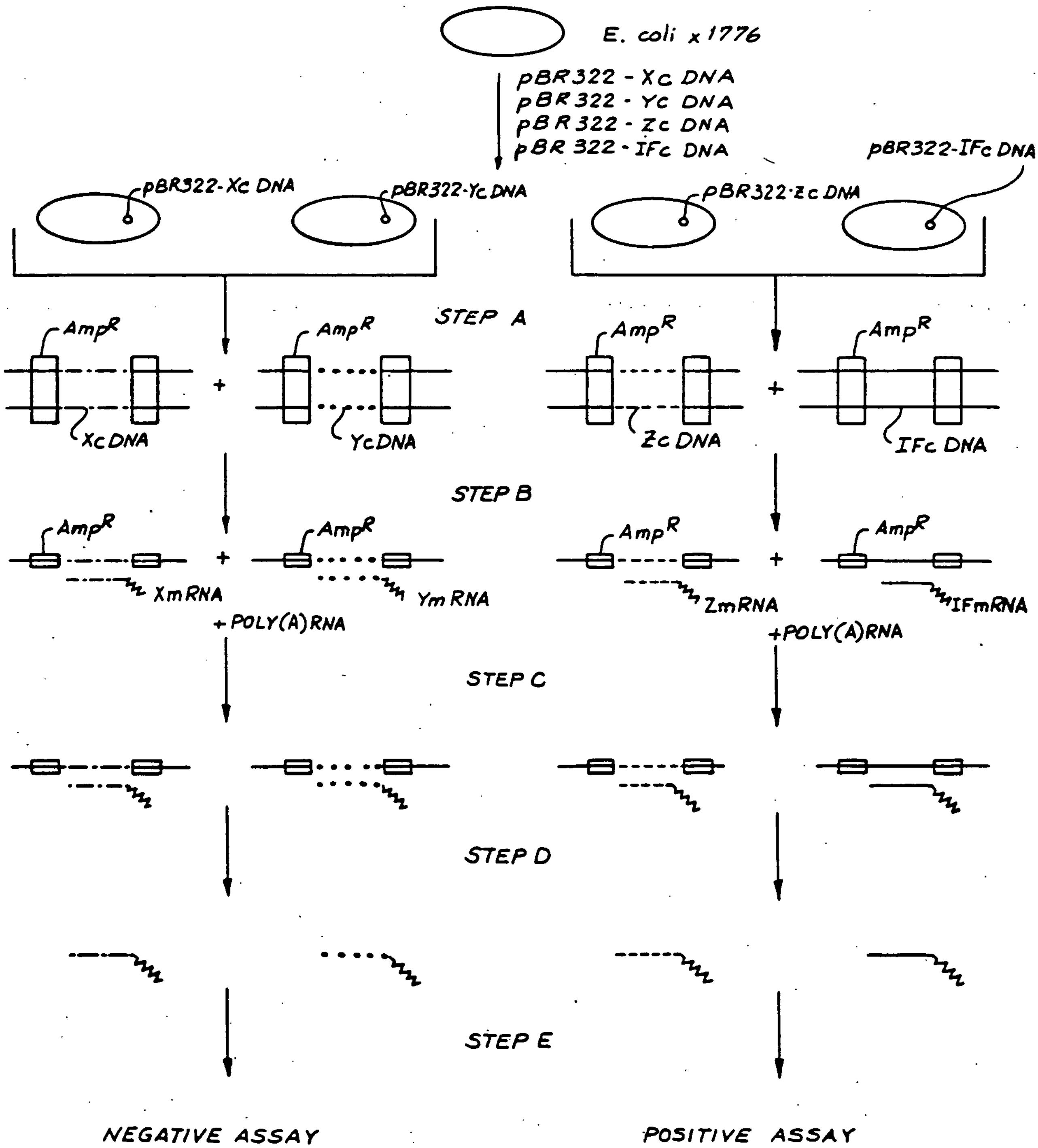

HUMAN LEUKOCYTES
SENDAI VIRUS
INDUCED HUMAN LEUKOCYTES
EXTRACTION
OLIGO (dT) CELLULOSE
Zm RNA
Xm RNA
Ym RNA
POLY (A) RNA
IFm RNA
REVERSE TRANSCRIPTASE
Zc DNA
Xc DNA
Yc DNA
IFc DNA
DNA POLYMERASE I
S1 NUCLEASE
dCTP/TERMINAL DEOXYNUCLEOTIDYL TRANSFERASE
CCC
3'
5'
Eco RI
Pst I
AmpR
Hind II
Taq
Bam I
pBR 322
TetR
Pvu II
(1) Pst I
(2) dGTP/TERMINAL DEOXYNUCLEOTIDYL TRANSFERASE
GGG
pBR322-Zc DNA
pB322-Yc DNA
pB322-IFc DNA
pB322-Xc DNA

FIG. 2


E. coli x 1776
pBR322 - Xc DNA
pBR322 - Yc DNA
pBR322 - Zc DNA
pBR322 - IFc DNA
pBR322-Xc DNA
pBR322-Yc DNA
pBR322-Zc DNA
pBR322-IFc DNA
STEP A
AmpR
Xc DNA
Yc DNA
Zc DNA
IFc DNA
STEP B
Xm RNA
Ym RNA
Zm RNA
IFm RNA
+POLY(A)RNA
STEP C
STEP D
STEP E
NEGATIVE ASSAY
POSITIVE ASSAY

7487280

FIG. 3

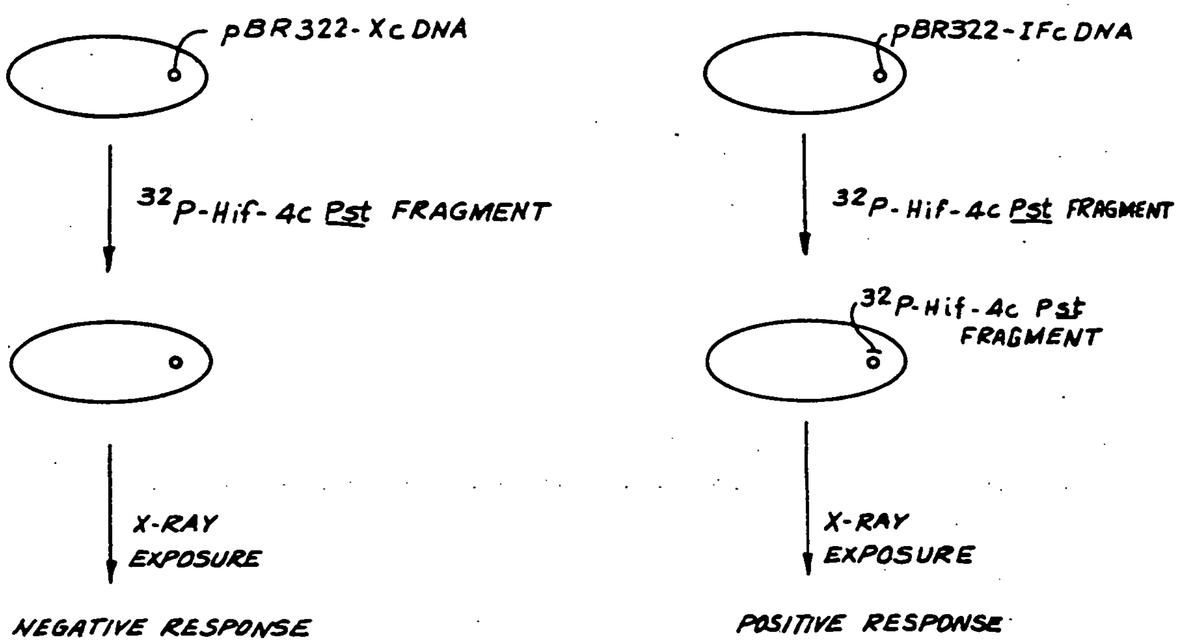


FIG. 4

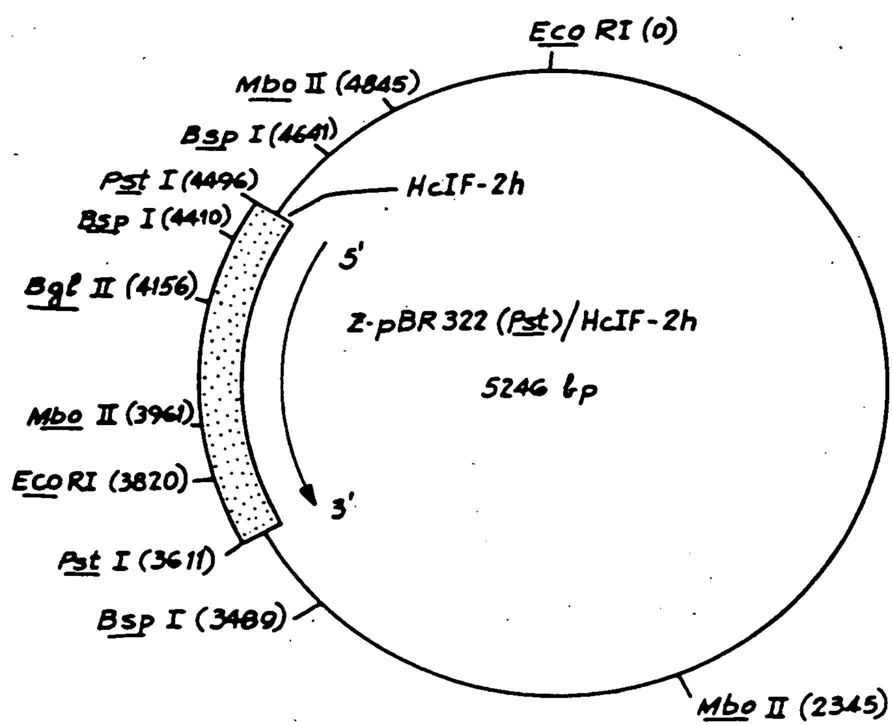
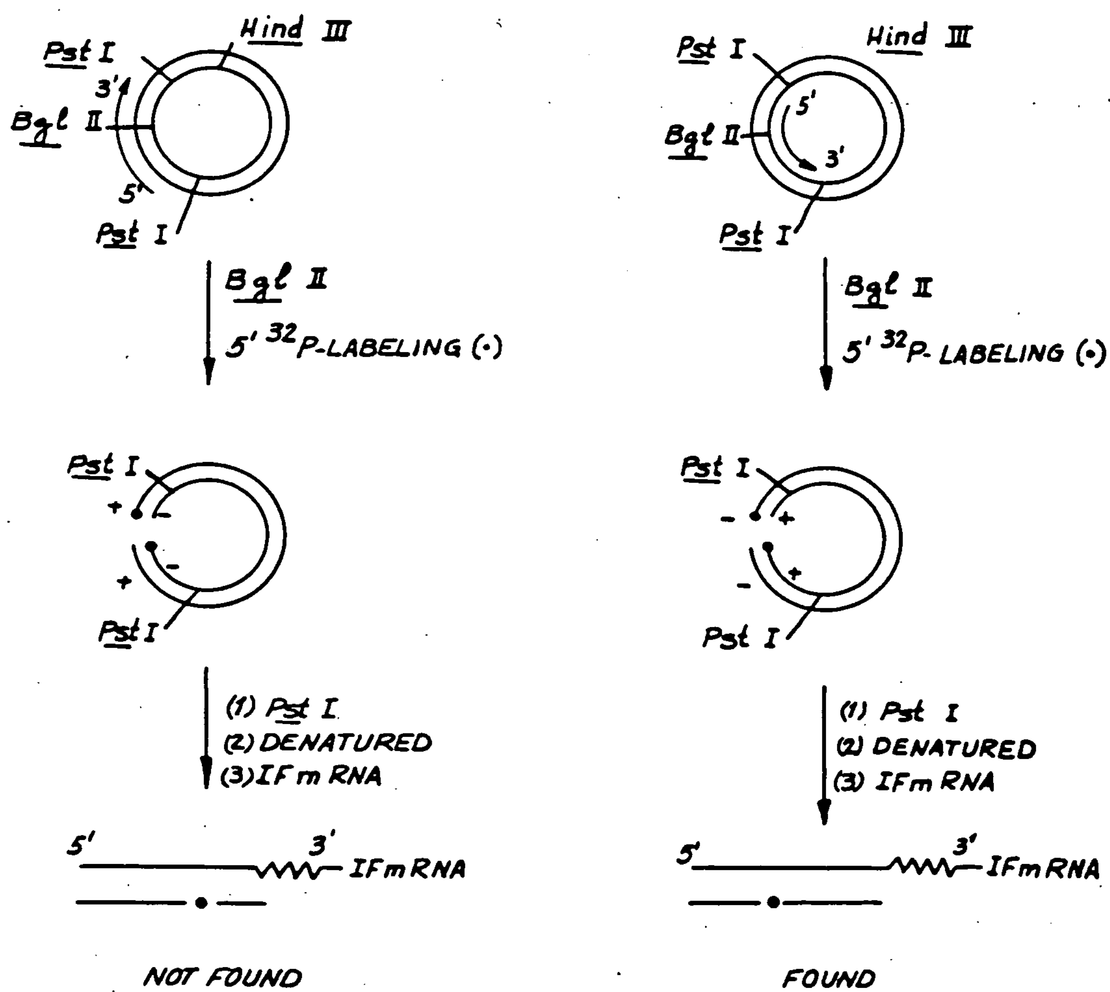


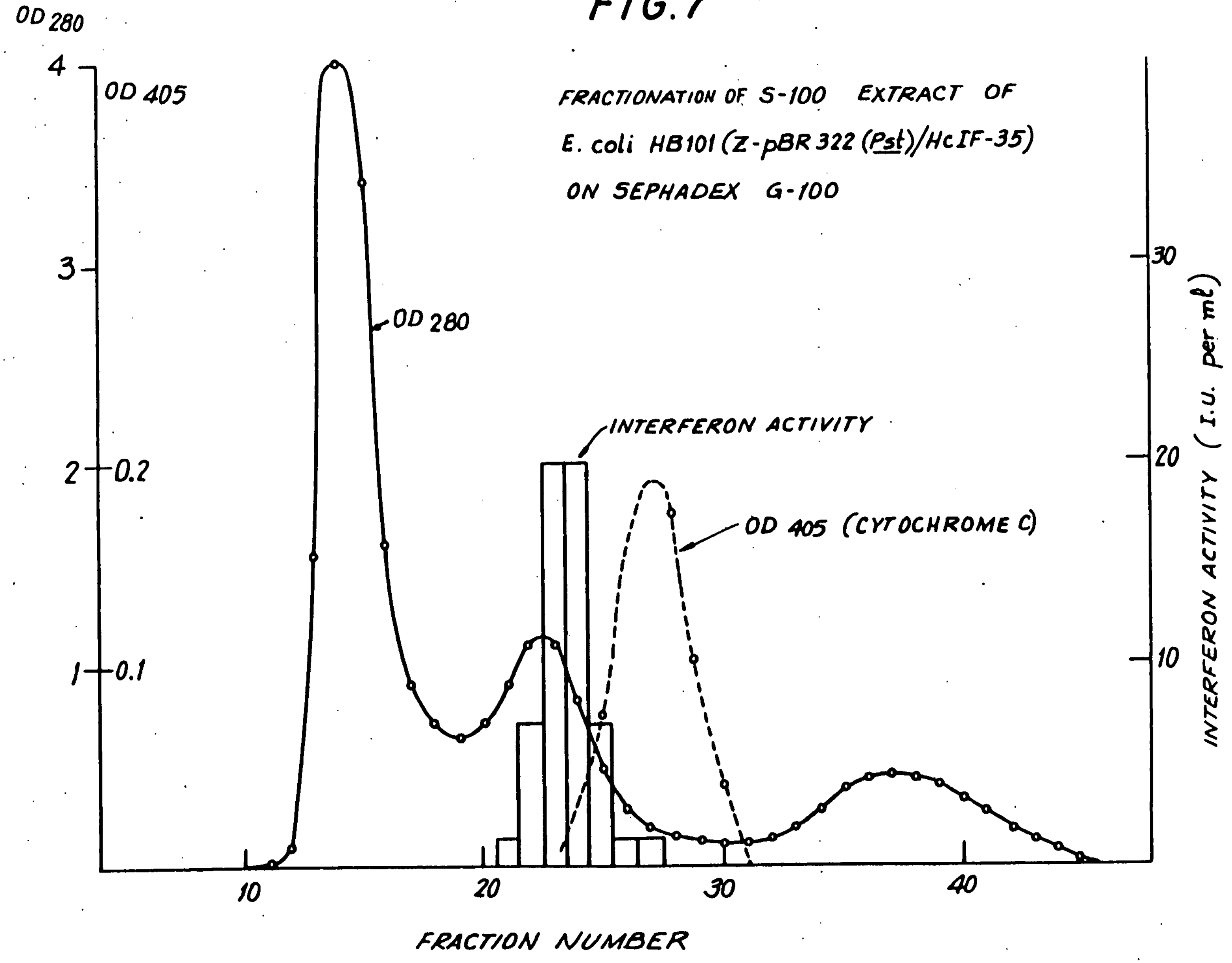
FIG. 5


Pst I
Hind III
3'
Bgl II
5'
Pst I
Bgl II
5' 32P-LABELING (•)
Pst I
+
-
Pst I
(1) Pst I
(2) DENATURED
(3) IF m RNA
5'
3'
IFmRNA
NOT FOUND
Pst I
Hind III
5'
Bgl II
3'
Pst I
Bgl II
5' 32P-LABELING (•)
Pst I
-
+
Pst I
(1) Pst I
(2) DENATURED
(3) IFm RNA
5'
3'
IFmRNA
FOUND

```
                               10                                       20
       MetSerIleGlnHisPheArgValAlaLeuIleProPhePheAlaAlaPheCysLeuProValPheAlaHisProGluThr
pBR322 ATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACG
         29     181
       LeuVal   ProAlaAlaMet
       CTGGTG···CCTGCAGCAATG···
                  Pst

                                                                                  24
       MetSerIleGlnHisPheArgValAlaLeuIleProPhePheAlaAlaPheCysLeuProValPheAlaHisArgCysSerAsn
pKT279 ATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCGCTGCAGCAATG···
                                                                                    Pst

                                                                                     25
       MetSerIleGlnHisPheArgValAlaLeuIleProPhePheAlaAlaPheCysLeuProValPheAlaHisProLeuGlnGln
pKT280 ATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCGCTGCAGCAATG···
                                                                                     Pst

                                                                                     27
       MetSerIleGlnHisPheArgValAlaLeuIleProPhePheAlaAlaPheCysLeuProValPheAlaHisProGluThr
pKT287 ATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACG··

       AlaAlaAlaMet
       GCTGCAGCAATG···
        Pst
```

FIG 6

FIG.7


OD 280
OD 405
4
3
2
0.2
1
0.1
FRACTIONATION OF S-100 EXTRACT OF
E. coli HB101 (Z-pBR 322 (Pst)/HcIF-35)
ON SEPHADEX G-100
OD 280
INTERFERON ACTIVITY
OD 405 (CYTOCHROME C)
30
20
10
INTERFERON ACTIVITY (I.U. per ml)
10
20
30
40
FRACTION NUMBER

nr/487280

```
                                                                    S1                         S10
1       10        20        30        40        50        60        70        80
                                                                    METALASERPROPHEALALEULEUMETVALLEU
G23CTCTAGGTTCAGAGTCACCCATCTCAGCAAGCCCAGAAGTATCTGCAATATCTACGATGGCCTCGCCCTTTGCTTTACTGATGGTCCTG
          HINF                                                BSPI                       ECORII
                                                                                       AVAII

                  S20           1                    10
90      100       110      120      130      140      150      160      170
VALVALLEUSERCYSLYSSERSERCYSSERLEUGLYCYSASPLEUPROGLUTHRHISSERLEUASPASNARGARGTHRLEUMETLEULEU
GTGGTGCTCAGCTGCAAGTCAAGCTGCTCTCTGGGCTGTGATCTCCCTGAGACCCACAGCCTGGATAACAGGAGGACCTTGATGCTCCTG
    DDEI  PVUII    ALUI              MBOI  DDEI ECOPI   ECORII        AVAII  SFANI ECORII
        ALUI

20                         30                      40
180     190       200      210      220      230      240      250      260
ALAGLNMETSERARGILESERPROSERSERCYSLEUMETASPARGHISASPPHEGLYPHEPROGLNGLUGLUPHEASPGLYASNGLNPHE
GCACAAATGAGCAGAATCTCTCCTTCCTCCTGTCTGATGGACAGACATGACTTTGGATTTCCCCAGGAGGAGTTTGATGGCAACCAGTTC
            HINF                                             ECORII
```

FIG. 8

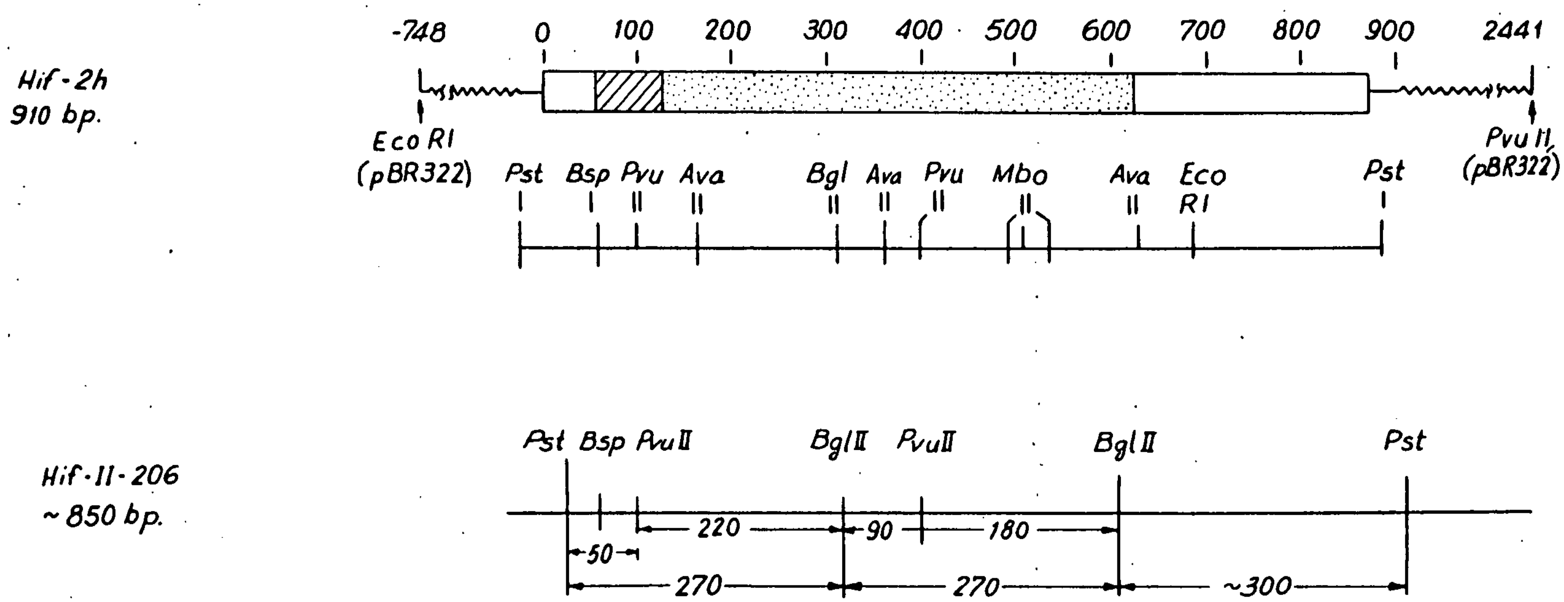
```
50                                                 60                                                70
270          280          290          300          310          320          330          340          350
GLNLYSALAPROALAILESERVALLEUHISGLULEUILEGLNGLNILEPHEASNLEUPHETHRTHRLYSASPSERSERALAALATRPASP
CAGAAGGCTCCAGCCATCTCTGTCCTCCATGAGCTGATCCAGCAGATCTTCAACCTCTTTACCACAAAAGATTCATCTGCTGCTTGGGAT
                              ALUMBOI /  BGLII                          HINF
                                 EcoP15
                                         MBOI MBOII

80                                                 90                                                100
360          370          380          390          400          410          420          430          440
GLUASPLEULEUASPLYSPHECYSTHRGLULEUTYRGLNGLNLEUASNASPLEUGLUALACYSVALMETGLNGLUGLUARGVALGLYGLU
GAGGACCTCCTAGACAAATTCTGCACCGAACTCTACCAGCAGCTGAATGACTTGGAAGCCTGTGTGATGCAGGAGGAGAGGGTGGGAGAA
  AVAII                                 EcoP15 PVUII                      SFANI
                                               ALUI

110                                                120                                               130
450          460          470          480          490          500          510          520          530
THRPROLEUMETASNALAASPSERILELEUALAVALLYSLYSTYRPHEARGARGILETHRLEUTYRLEUTHRGLULYSLYSTYRSERPRO
ACTCCCCTGATGAATGCGGACTCCATCTTGGCTGTGAAGAAATACTTCCGAAGAATCACTCTCTATCTGACAGAGAAGAAATACAGCCCT
                   HINF                MBOII      MBOII                       MBOII
                                                     HINF
```

FIG.9

```
 140                          150                           160               166
540       550       560       570       580       590       600       610       620
CYSALATRPGLUVALVALARGALAGLUILEMETARGSERLEUSERLEUSERTHRASNLEUGLNGLUARGLEUARGARGLYSGLU
TGTGCCTGGGAGGTTGTCAGAGCAGAAATCATGAGATCCCTCTCTTTATCAACAAACTTGCAAGAAAGATTAAGGAGGAAGGAATAACAT
    EcoRII                        MboI

630       640       650       660       670       680       690       700       710
CTGGTCCAACATGAAAACAATTCTTATTGACTCATACACCAGGTCACGCTTTCATGAATTCTGTCATTTCAAAGACTCTCACCCCTGCTA
  AvaII                     Hinf     EcoRII            EcoRI              Hinf  Hph

720       730       740       750       760       770       780       790       800
TAACTATGACCATGCTGATAAACTGATTTATCTATTTAAATATTTATTTAACTATTCATAAGATTTAAATTATTTTTGTTCATATAACGT

810       820       830       840       850       860  865
CATGTGCACCTTTACACTGTGGTTAGTGTAATAAAACATGTTCCTTATATTTACTCAAAAAAAC15
   AccI
```

FIG. 10

FIG. 11


Hif-2h
910 bp.
-748
0
100
200
300
400
500
600
700
800
900
2441
Eco RI
(pBR322)
Pvu II
(pBR322)
Pst
Bsp
Pvu
Ava
Bgl
Ava
Pvu
Mbo
Ava
Eco RI
Pst
Hif-II-206
~850 bp.
Pst
Bsp
PvuII
BglII
PvuII
BglII
Pst
220
90
180
50
270
270
~300

```
                                                                        -50       -40
206(II)                                                           G13 TTACTGGTGGCCCTC
                                                                    leu leu val ala leu
                                                              -20
                                                   met ala ser pro phe ala leu leu met val leu
2H(I)   G23 CTCTAGGTTCAGAGTCACCCATCTCAGCAAGCCCAGAAGTATCTGCAATATCTACGATGGCCTCGCCCTTTGCTTTACTGATGGTCCTG
              -120     -110     -100     -90      -80      -70      -60      -50      -40

          -30      -20      -10       1       10       20       30       40       50
206(II)  CTGGTGCTCAGCTGCAAGTCAAGCTGCTCTGTGGGCTGTGATCTGCCTCAAACCCACAGCCTGGGTAGCAGGAGGACCTTGATGCTCCTG
         leu val leu ser cys lys ser ser cys ser val gly CYS ASP LEU PRO GLN THR HIS SER LEU GLY SER ARG ARG THR LEU MET LEU LEU
          -10                          -1  1                   10
         val val leu ser cys lys ser ser cys ser leu gly CYS ASP LEU PRO GLU THR HIS SER LEU ASP ASN ARG ARG THR LEU MET LEU LEU
2H(I)    GTGGTGCTCAGCTGCAAGTCAAGCTGCTCTCTGGGCTGTGATCTCCCTGAGACCCACAGCCTGGATAACAGGAGGACCTTGATGCTCCTG
          -30      -20      -10       1       10       20       30       40       50
```

FIG. 12

```
                60        70        80        90        100       110       120          130       140
206(II)   GCACAGATGAGGAGAATCTCTCTTTTCTCCTGCTTGAAGGACAGACATGACTTTGGATTTCCCCAGGAGGAGTTT---GGCAACCAGTTC
          ALA GLN MET ARG ARG ILE SER LEU PHE SER CYS LEU LYS ASP ARG HIS ASP PHE GLY PHE PRO GLN GLU GLU PHE - GLY ASN GLN PHE

          20                            30                            40
          ALA GLN MET SER ARG ILE SER PRO SER SER CYS LEU MET ASP ARG HIS ASP PHE GLY PHE PRO GLN GLU GLU PHE ASP GLY ASN GLN PHE
2H(I)     GCACAAATGAGCAGAATCTCTCCTTCCTCCTGTCTGATGGACAGACATGACTTTGGATTTCCCCAGGAGGAGTTTGATGGCAACCAGTTC
                60        70        80        90        100       110       120       130       140


                150       160       170       180       190       200       210       220       230
206(II)   CAAAAGGCTGAAACCATCCCTGTCCTCCATGAGATGATCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTTGGGAT
          GLN LYS ALA GLU THR ILE PRO VAL LEU HIS GLU MET ILE GLN GLN ILE PHE ASN LEU PHE SER THR LYS ASP SER SER ALA ALA TRP ASP
              50                            60                            70
          50                            60                            70
          GLN LYS ALA PRO ALA ILE SER VAL LEU HIS GLU LEU ILE GLN GLN ILE PHE ASN LEU PHE THR THR LYS ASP SER SER ALA ALA TRP ASP
2H(I)     CAGAAGGCTCCAGCCATCTCTGTCCTCCATGAGCTGATCCAGCAGATCTTCAACCTCTTTACCACAAAAGATTCATCTGCTGCTTGGGAT
              150       160       170       180       190       200       210       220       230
```

FIG. 13

```
                 240       250       260       270       280       290       300       310       320
206(II)   GAGACCCTCCTAGACAAATTCTACACTGAACTCTACCAGCAGCTGAATGACCTGGAAGCCTGTGTGATACAGGGGGTGGGGGTGACAGAG
          GLU THR LEU LEU ASP LYS PHE TYR THR GLU LEU TYR GLN GLN LEU ASN ASP LEU GLU ALA CYS VAL ILE GLN GLY VAL GLY VAL THR GLU
                 80                            90                            100

              80                            90                            100
          GLU ASP LEU LEU ASP LYS PHE CYS THR GLU LEU TYR GLN GLN LEU ASN ASP LEU GLU ALA CYS VAL MET GLN GLU GLU ARG VAL GLY GLU
2H(I)     GAGGACCTCCTAGACAAATTCTGCACCGAACTCTACCAGCAGCTGAATGACTTGGAAGCCTGTGTGATGCAGGAGGAGAGGGTGGGAGAA
             240       250       260       270       280       290       300       310       320

                 330       340       350       360       370       380       390       400       410
206(II)   ACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAAATACTTCCAAAGAATCACTCTCTATCTGAAAGAGAAGAAATACAGCCCT
          THR PRO LEU MET LYS GLU ASP SER ILE LEU ALA VAL ARG LYS TYR PHE GLN ARG ILE THR LEU TYR LEU LYS GLU LYS LYS TYR SER PRO
                 110                           120                           130

              110                           120                           130
          THR PRO LEU MET ASN ALA ASP SER ILE LEU ALA VAL LYS LYS TYR PHE ARG ARG ILE THR LEU TYR LEU THR GLU LYS LYS TYR SER PRO
2H(I)     ACTCCCCTGATGAATGCGGACTCCATCTTGGCTGTGAAGAAATACTTCCGAAGAATCACTCTCTATCTGACAGAGAAGAAATACAGCCCT
             330       340       350       360       370       380       390       400       410
```

FIG. 14

```
              420       430       440       450       460       470       480       490       500
206(II)   TGTGCCTGGGAGGTTGTCAGAGCAGAAATCATGAGATCTTTTTCTTTGTCAACAAACTTGCAAGAAAGTTTAAGAAGTAAGGAATGAAAA
          CYS ALA TRP GLU VAL VAL ARG ALA GLU ILE MET ARG SER PHE SER LEU SER THR ASN LEU GLN GLU SER LEU ARG SER LYS GLU
              140                                     150                                         160           165

           140                                    150                                         160           166
          CYS ALA TRP GLU VAL VAL ARG ALA GLU ILE MET ARG SER LEU SER LEU SER THR ASN LEU GLN GLU ARG LEU ARG ARG LYS GLU
2H(I)     TGTGCCTGGGAGGTTGTCAGAGCAGAAATCATGAGATCCCTCTCTTTATCAACAAACTTGCAAGAAAGATTAAGGAGGAAGGAATAACAT
            420       430       440       450       460       470       480       490       500


              510       520       530       540       550         560       570       580
206(II)   CTGGTTCAACATGGAAATGATTTTCATTGATTCGTATGCCAGCTCACCTTTTTATGA--TCTGCCATTTCAAAGACTCATGTTTCTGCTA

2H(I)     CTGGTCCAACATGAAAACAATTCTTATTGACTCATACACCAGGTCACGCTTTCATGAATTCTGTCATTTCAAAGACTCTCACCCCTGCTA
            510       520       530       540       550       560       570       580       590
```

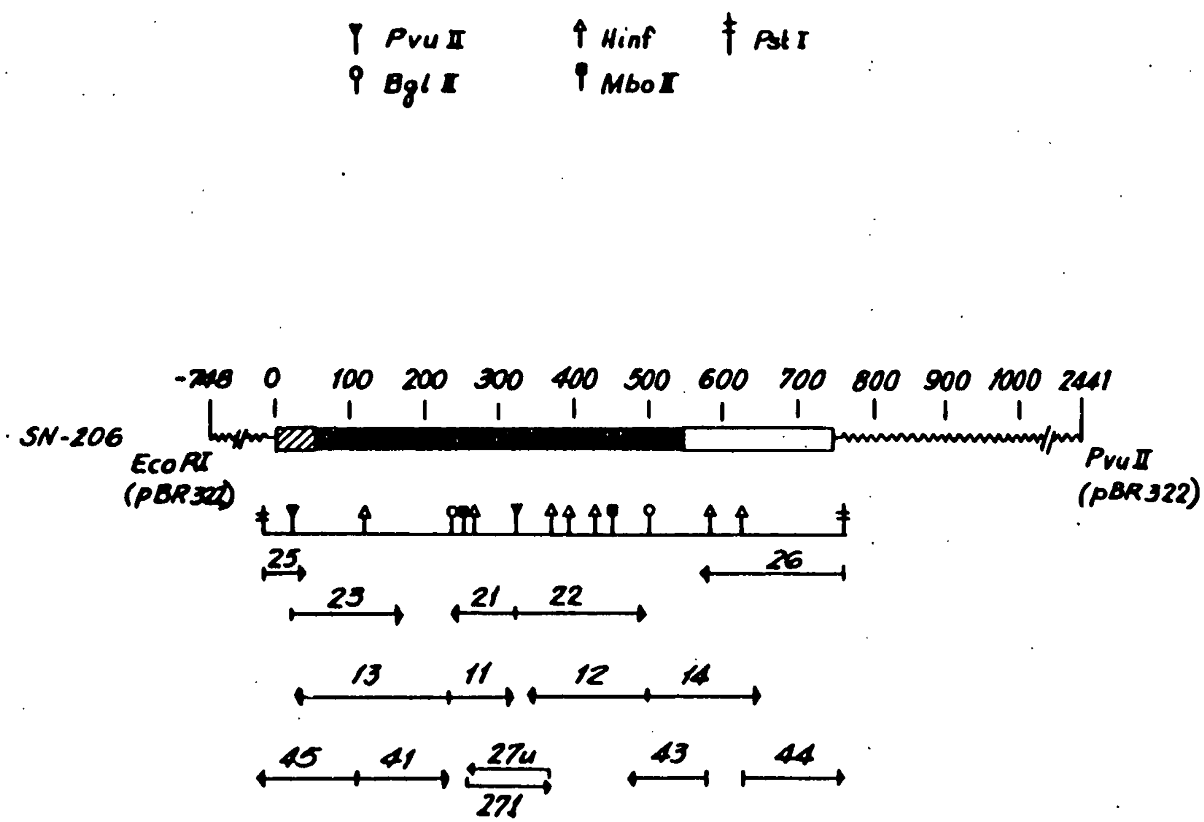
FIG. 15

```
        590       600       610       620       630       640       650       660       670       680
206(II) TGACCATGACACGATTTAAATCTTTTCAAATGTTTTTAGGAGTATTAATCAACATTGTATTCAGCTCTTAAGGCACTAGTCCCTTACAGAG

2H(I)   TAACTATGACCATGCTGATAAACTGATTTATCTATTTAAATATTTATTTAACTATTCATAAGATTTAAATTATTTTTGTTCATATAACGTC
            600       610       620       630       640       650       660       670       680
```

```
              690
206(II) GACCATGCTGAC29

2H(I)   ATGTGCACCTTTACACTGTGGTTAGTGTAATAAAACATGTTCCTTATATTTACTCAAAAAAAC15
           690       700       710       720       730       740
```

FIG. 16

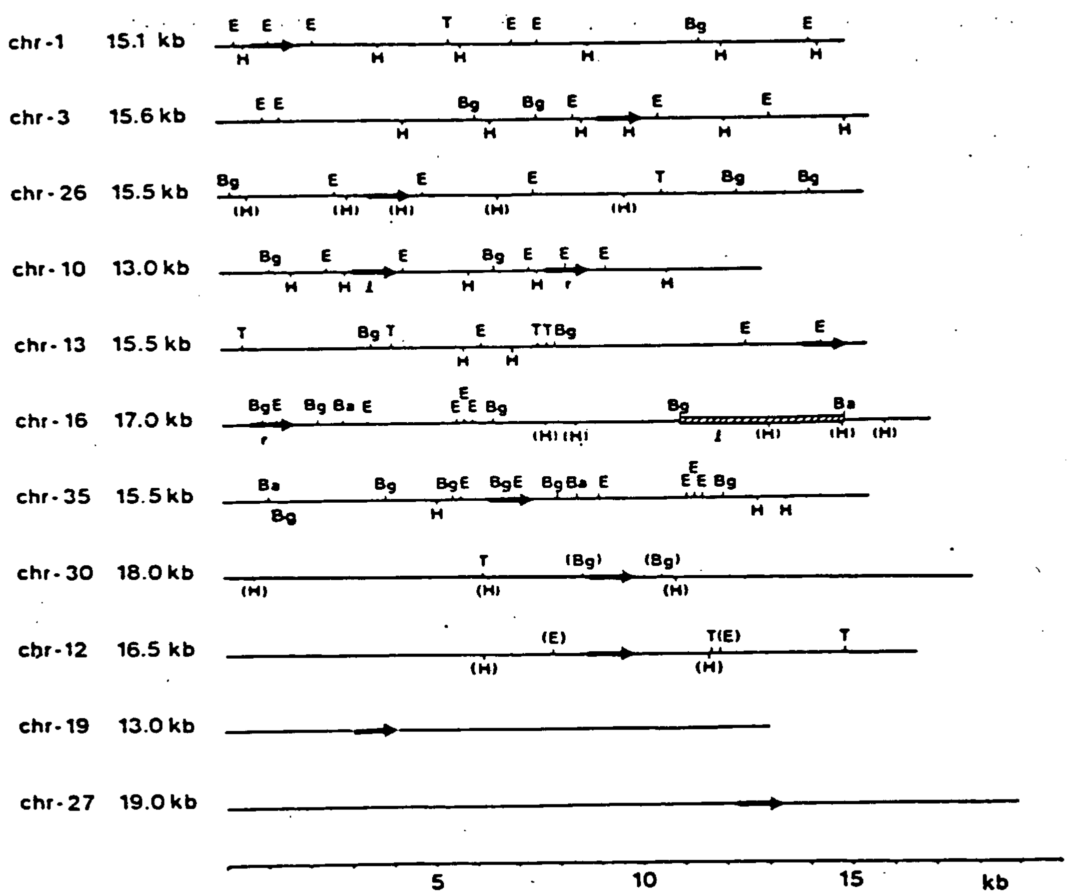
FIG. 17



Pvu II
Bgl II
Hinf
Mbo II
Pst I
-748
0
100
200
300
400
500
600
700
800
900
1000
2441
SN-206
EcoRI
(pBR322)
Pvu II
(pBR322)
25
26
23
21
22
13
11
12
14
45
41
27u
27l
43
44

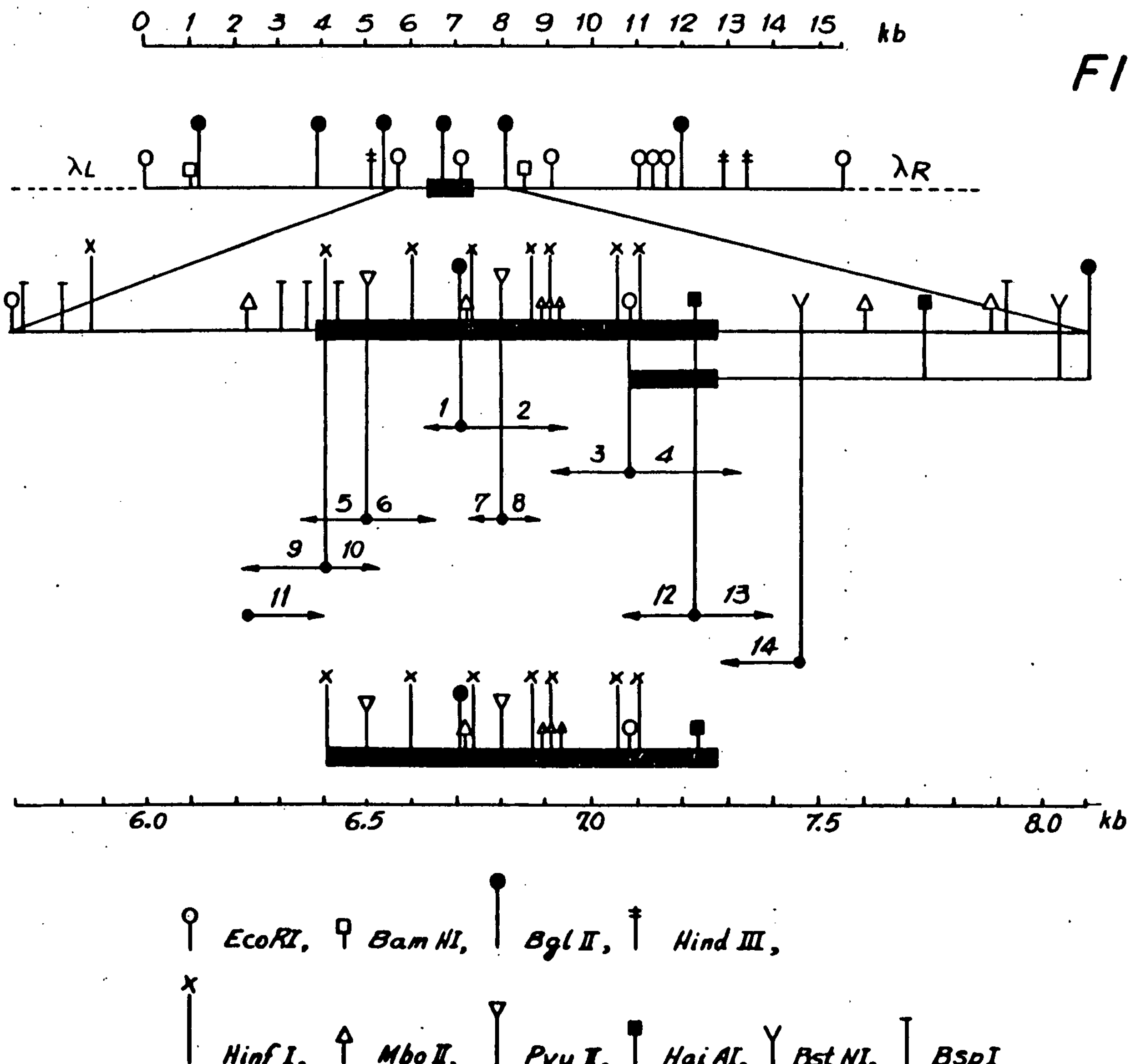
FIG. 18

PARTIAL RESTRICTION MAPS OF CLONED, IFN-α RELATED CHROMOSOMAL DNA SEGMENTS



E : EcoRI, Ba : BamHI, Bg : BglII, H : HincII, T : TacI

FIG. 19



0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 kb
λL
λR
1 2
3 4
5 6
7 8
9 10
11
12 13
14
6.0 6.5 7.0 7.5 8.0 kb
EcoRI, BamHI, BglII, HindIII,
HinfI, MboII, PvuII, HgiAI, BstNI, BspI

AAAACAAAACATTTGAGAAACACGGCTCTAAACTCATGTAAAGAGTGCATGAAGGAAAGCAAAAACAGAAATG

-140 -120 -100 -80 -60

GAAAGTGGCCCAGAAGCATTAAGAAAGTGGAAATCAGTATGTTCCCTATTTAAGGCATTTGCAGGAAGCAAGGCCTTCAGAGAACCTAGA

BspI BspI

S1 S10

-40 -20 +1 20

metalaserprophealaleuleumetvalleu

GCCCAAGGTTCAGAGTCACCCATCTCAGCAAGCCCAGAAGTATCTGCAATATCTACGATGGCCTCGCCCTTTGCTTTACTGATGGTCCTG

HinF BspI EcoRII

AvaII

S20 1 10

40 60 80 100 120

valvalleuserOySlysserserOyserleuglyCYSASPLEUPROGLUTHRHISSERLEUASPASNARGARGTHRLEUMETLEULEU

GTGGTGCTCAGCTGCAAGTCAAGCTGCTCTCTGGGCTGTGATCTCCCTGAGACCCACAGCCTGGATAACAGGAGGACCTTGATGCTCCTG

DdeI PvuII AluI MboI DdeI EcoPI EcoRII AvaII SfaNI EcoRII

AluI

FIG. 20

```
20                            30                             40
            140                     160                    180                    200
ALAGLNMETSERARGILESERPROSERSERCYSLEUMETASPARGHISASPPHEGLYPHEPROGLNGLUGLUPHEASPGLYASNGLNPHE
GCACAAATGAGCAGAATCTCTCCTTCCTCCTGTCTGATGGACAGACATGACTTTGGATTTCCCCAGGAGGAGTTTGATGGCAACCAGTTC
             HINF                                                   EcoRII

50                            60                             70
  220                   240                     260                    280                    300
GLNLYSALAPROALAILESERVALLEUHISGLULEUILEGLNGLNILEPHEASNLEUPHETHRTHRLYSASPSERSERALAALATRPASP
CAGAAGGCTCCAGCCATCTCTGTCCTCCATGAGCTGATCCAGCAGATCTTCAACCTCTTTACCACAAAAGATTCATCTGCTGCTTGGGAT
                                ALU MBOI/  BGLII                       HINF
                                    EcoP15
                                           MBOI MBOII

80                            90                            100
            320                     340                    360                    380
GLUASPLEULEUASPLYSPHECYSTHRGLULEUTYRGLNGLNLEUASNASPLEUGLUALACYSVALMETGLNGLUGLUARGVALGLYGLU
GAGGACCTCCTAGACAAATTCTGCACCGAACTCTACCAGCAGCTGAATGACTTGGAAGCCTGTGTGATGCAGGAGGAGAGGGTGGGAGAA
  AVAII                              EcoP15 PVUII                       SFANI
                                            ALUI
```

FIG. 21

110 120 130

400 420 440 460 480

THRPROLEUMETASNALAASPSERILELEUALAVALLYSLYSTYRPHEARGARGILETHRLEUTYRLEUTHRGLULYSLYSTYRSERPRO

ACTCCCCTGATGAATGCGGACTCCATCTTGGCTGTGAAGAAATACTTCCGAAGAATCACTCTCTATCTGACAGAGAAGAAATACAGCCCT

HINF MBOII MBOII HINF MBOII

140 150 160 166

500 520 540 560

CYSALATRPGLUVALVALARGALAGLUILEMETARGSERLEUSERLEUSERTHRASNLEUGLNGLUARGLEUARGARGLYSGLU

TGTGCCTGGGAGGTTGTCAGAGCAGAAATCATGAGATCCCTCTCTTTATCAACAAACTTGCAAGAAAGATTAAGGAGGAAGGAATAACAT

EcoRII MBOI

580 600 620 640 660

CTGGTCCAACATGAAAACAATTCTTATTGACTCATACACCAGGTCACGCTTTCATGAATTCTGTCATTTCAAAGACTCTCACCCCTGCTA

AvaII HINF EcoRII EcoRI HINF HPH

680 700 720 740

TAACTATGACCATGCTGATAAACTGATTTATCTATTTAAATATTTATTTAACTATTCATAAGATTTAAATTATTTTTGTTCATATAACGT

760 780 800 820 840

CATGTGCACCTTTACACTGTGGTTAGTGTAATAAAACATGTTCCTTATATTTACTCAATCCATTATTTTGTGTTGTTCATTAAACTTTTA

HGIA

FIG. 22

```
               860                 880                 900                 920
CTATAGGAACTTCCTGTATGTGTTCATTCTTTAATATGAAATTCCTAGCCTGACTGTGCAACCTGATTAGAGAATAAAGGGTATATTTTA

       940                 959
TTTGCTTATCATTATTATATGTAAGA
```

FIG.23

FIG. 24

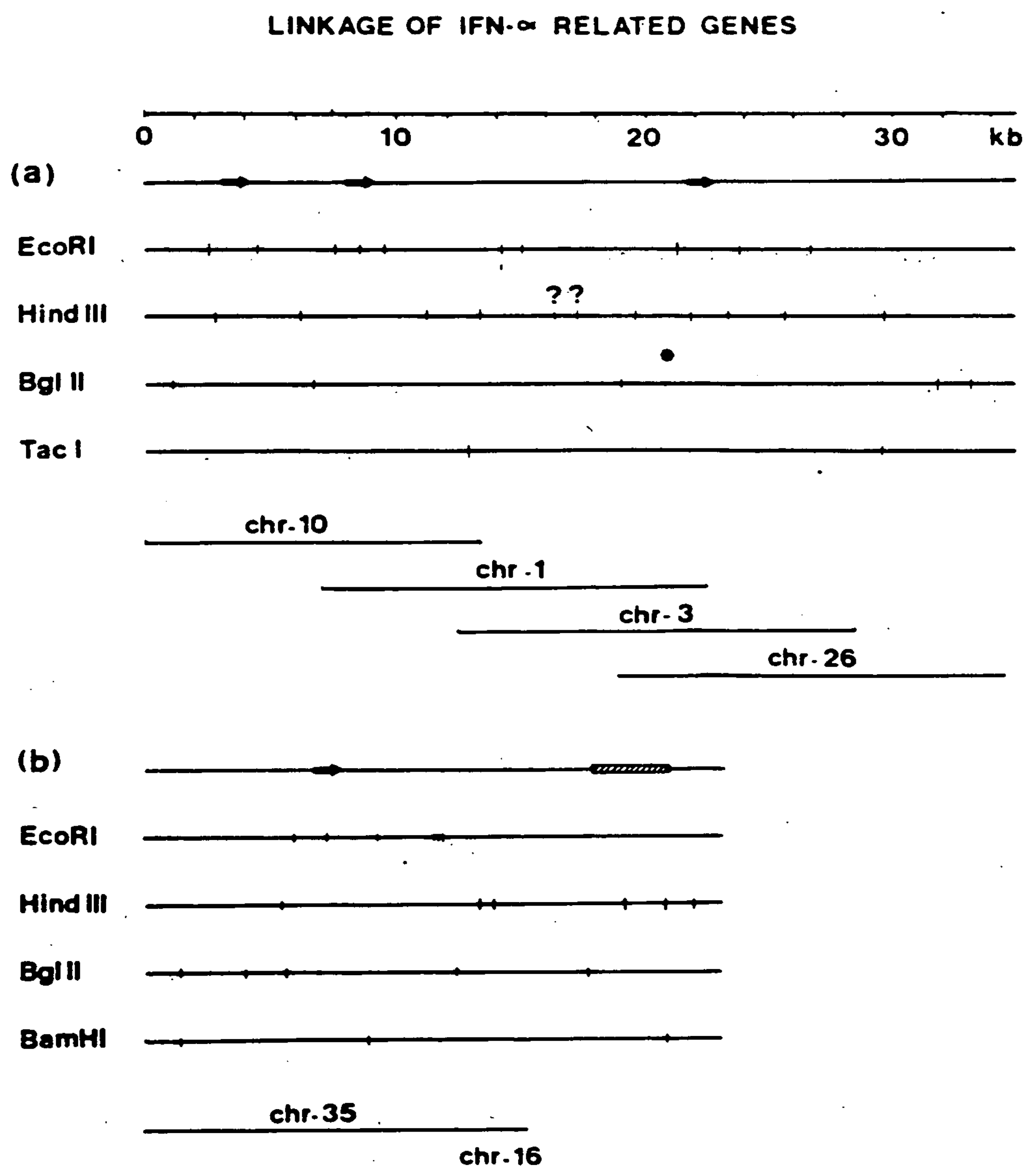
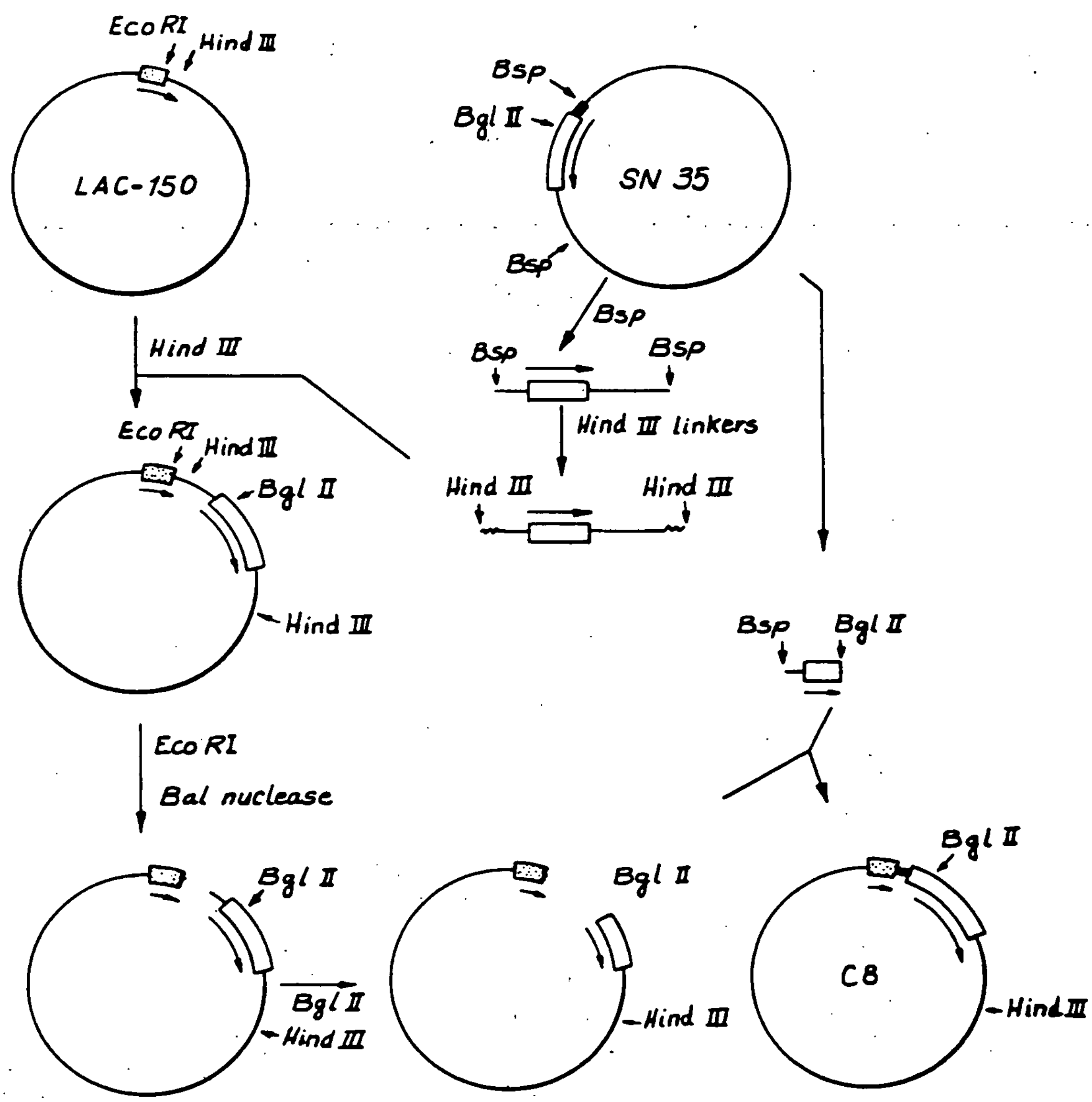

LINKAGE OF IFN-α RELATED GENES
0
10
20
30
kb
(a)
EcoRI
Hind III
??
Bgl II
Tac I
chr-10
chr-1
chr-3
chr-26
(b)
EcoRI
Hind III
Bgl II
BamHI
chr-35
chr-16

FIG. 25



Eco RI
Hind III
LAC-150
Bsp
Bgl II
SN 35
Bsp
Hind III
Bsp
Bsp
Bsp
Hind III linkers
Eco RI
Hind III
Bgl II
Hind III
Hind III
Hind III
Bsp
Bgl II
Eco RI
Bal nuclease
Bgl II
Bgl II
Hind III
Bgl II
Hind III
Bgl II
C8
Hind III

FIG. 26

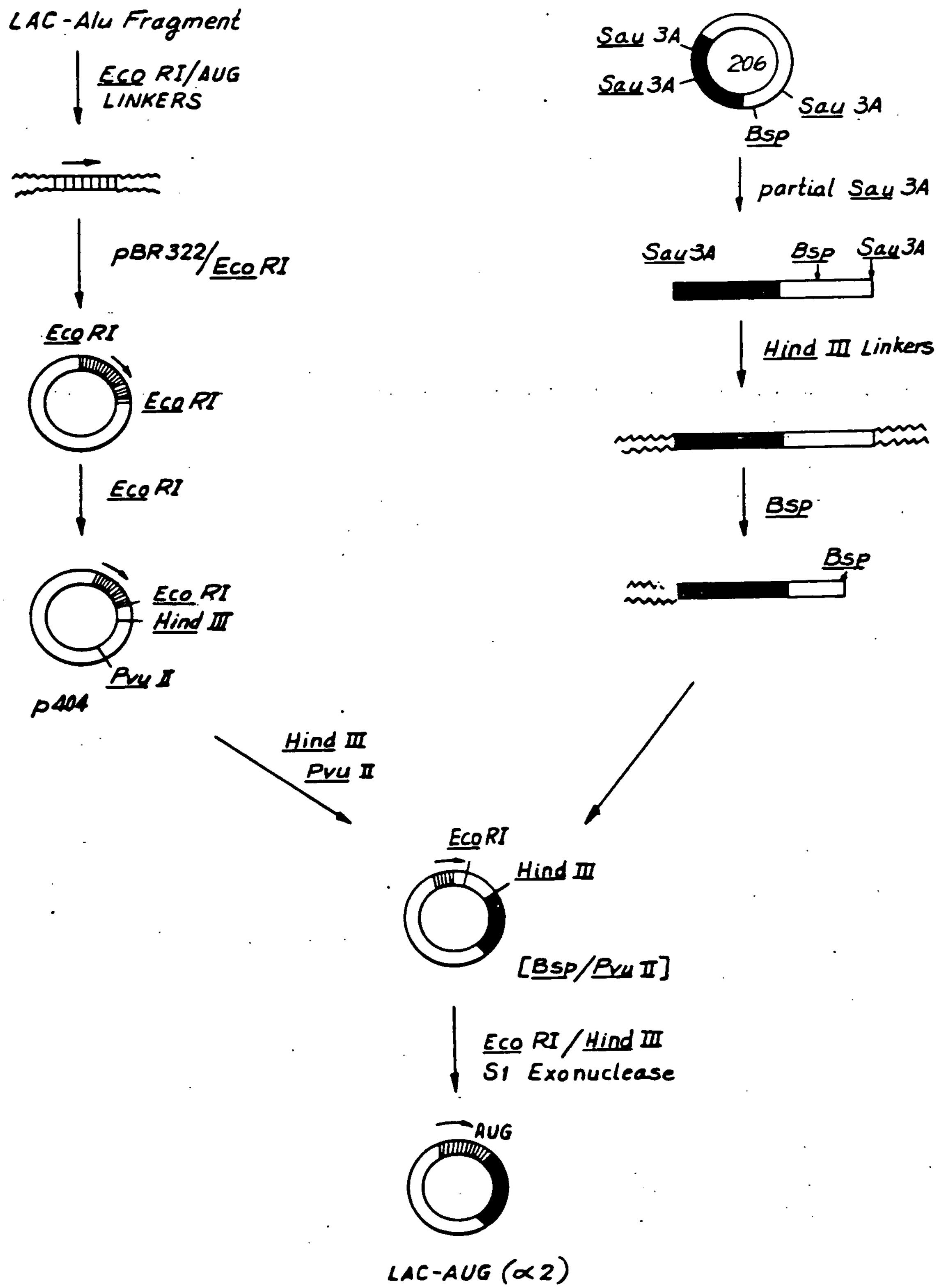

LAC-Alu Fragment
Eco RI/AUG
LINKERS
pBR322/Eco RI
Eco RI
Eco RI
Eco RI
Eco RI
Hind III
Pvu II
p404
Hind III
Pvu II
Sau 3A
206
Sau 3A
Sau 3A
Bsp
partial Sau 3A
Sau3A
Bsp
Sau3A
Hind III Linkers
Bsp
Bsp
Eco RI
Hind III
[Bsp/Pvu II]
Eco RI/Hind III
S1 Exonuclease
AUG
LAC-AUG (α2)

FIG. 27

CONSTRUCTION OF PLASMID LAC-AUG (α-2)

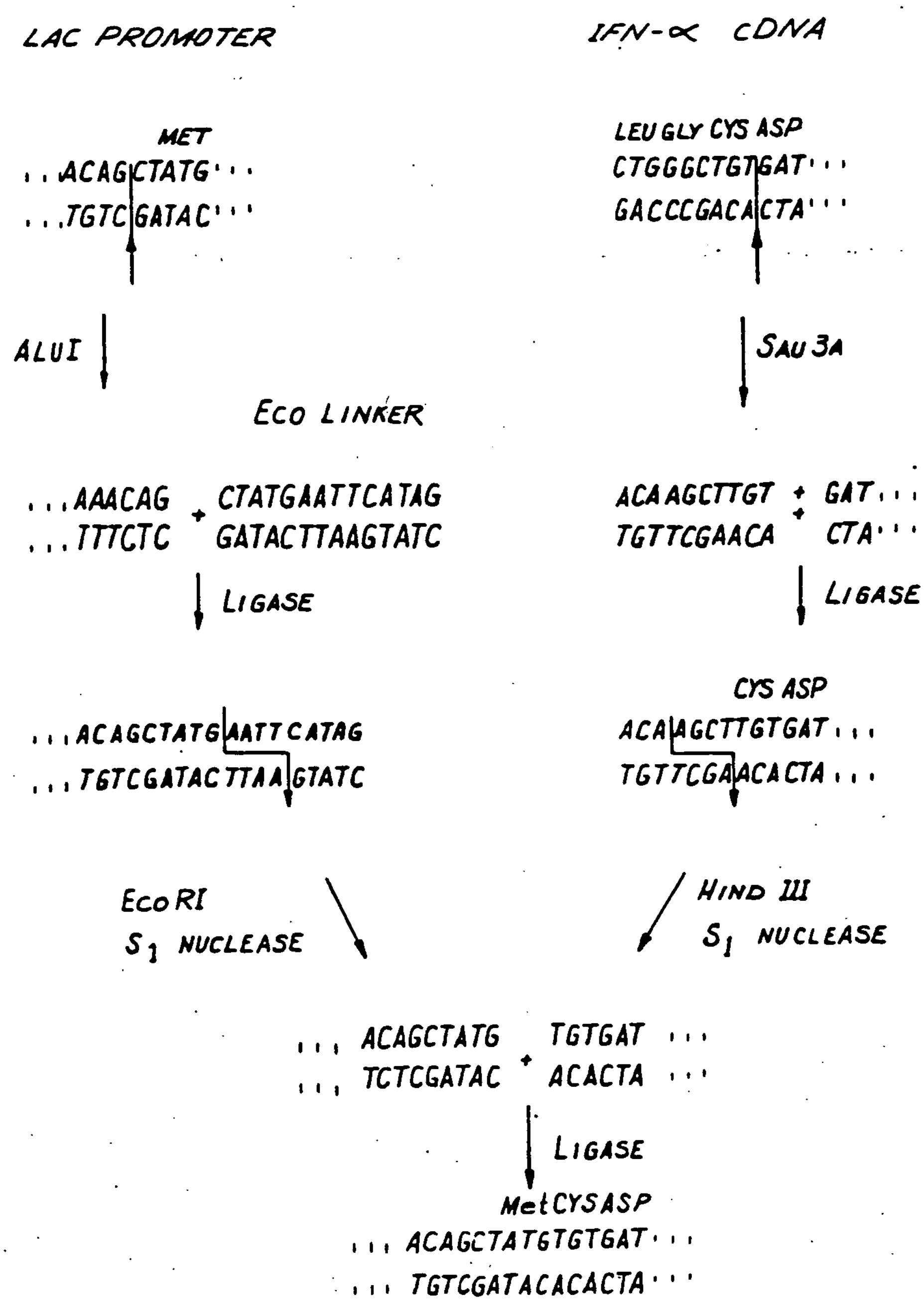
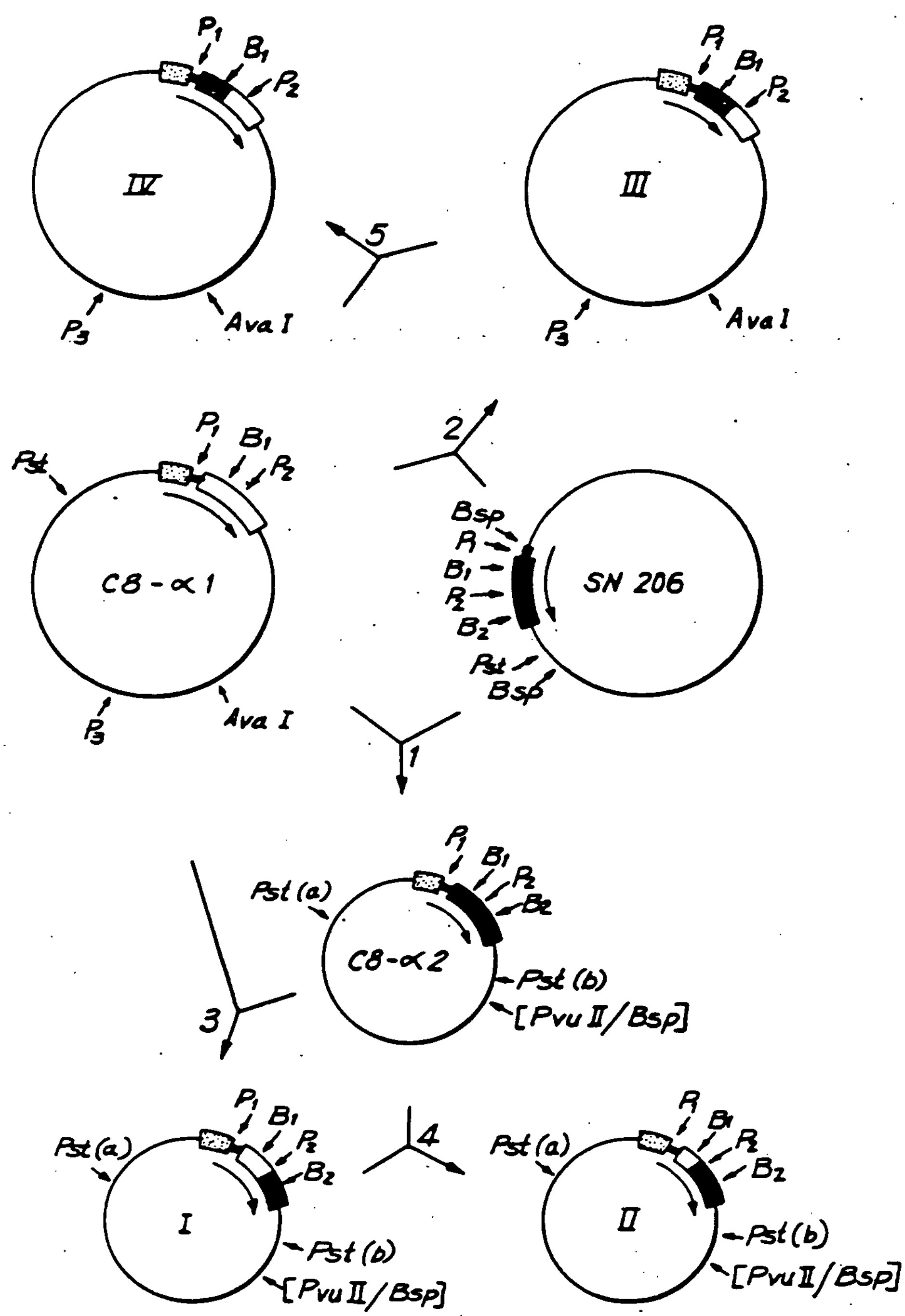


FIG. 28


P1
B1
P2
IV
P3
Ava I
5
P1
B1
P2
III
P3
Ava I
P1
B1
P2
Pst
C8-α1
P3
Ava I
2
Bsp
P1
B1
P2
B2
Pst
Bsp
SN 206
1
P1
B1
P2
B2
Pst (a)
C8-α2
Pst (b)
[Pvu II/Bsp]
3
P1
B1
P2
B2
Pst (a)
I
Pst (b)
[Pvu II/Bsp]
4
P1
B1
P2
B2
Pst (a)
II
Pst (b)
[Pvu II/Bsp]

```
                                                      160        180        200
                                                      C24AATGCAAATAGCTTATATTATATGATTTATTTCTAGTAAA
                                                                  AluI

         220        240        260        280        300
GTTATTCAACACATCAGTACTTATGTCAACTGCTGAAAAGAAAAAAGTGTTGGCAACATCTGGATGAATACTGCAGCTGATGAAGTTTACAAATTATTTT
                RsaI    ChuII                                          PstI
                                                                          AluI
                                                                         PvuII
                                                                        BbrsI

         320        340        360        380        400
GTCATATAAAGCAAAATTCAAAGCTTCATACACTAAGAGAAAAATTTTAAAAAATTATTCATTCATATTTTTAGGAGTTTTGAATGATTGGATATGTAAT
             EcoRI BbrI        DdeI   EcoRI
                    AluI

         420        440        460        480        500
TATATTCATATTATTAATGTGTATCTATATAGATTTTTATTTTGCATATGTACTTTGATACAAAATTTACATGAACAAATTACACTAAAGTTATTCCACA
                              EcoRI          RsaI      EcoRI

         520        540        560        580        600
ATATACTTATCAAATTAAGTTAATGTCAATAGCTTTTAAACTTAAATTTTAGTTTAGTTAGCTTTTCTGTCATTCTTACTTACTTTGAATAAAAAGAGCA
                              AluI       EcoRI       AluI
```

FIG. 29

```
                620        640        660        680        700
AACTTTGTAGTTTTTATCTCTGTGAAGTAGAGGTATACGTAATATACATAAATAGATATGCCAAATCTGTGTTATTAAAATTTCATGAAGATTTCAATTA
MalI   EcoRI   EcoRI   MboII

                720        740        760        780        800
GAAAAAAATACCATAAAAGGCTTTGAGTGCAGGTGAAAAATAGGCAATGATGAAAAAAAATGAAAAACTTTTTAAACACATGTGAGAGTGCGTAAGAAGC
HphI

                820        840        860        880        900
AAACAGAGATAGAAAGTACAACTAGGGAATTTAGAAAATGGAAATTAGTATGTTCACTATTTAAGACCTATGCACAGAGCAAAGTCTTCAGAAAACCTAG
RsaI   EcoRI   EcoRI   MboII

                920        940        960        980        1000
                                 metalaleuserpheserleuleumetalavalleuvalleuser
AGGCCGAAGTTCAAGGTTATCCATCTCAAGTAGCCCAGCAATATTTGCAACATCCAATGGCCCTGTCCTTTTCTTTACTGATGGCCGTGCTGGTGCTCAG
MnlI   BspI   AsuI   BspI   BspI   DdeI   AluI

                1020       1040       1060       1080       1100
tyrlysserilecysserleuglyCYSASPLEUPROGLNTHRHISSERLEUGLYASNARGARGTHRLEUILELEULEUGLNGLNMETGLYARGILESER
CTACAAATCCATCTGTTCTCTGGGCTGTGATCTGCCTCAGACCCACAGCCTGGGTAATAGGAGGACCTTGATACTCCTGCAACAAATGGGAAGAATCTCT
AluI   EcoRI   Dpn   MboI   MnlI   DdeI   BstNI   MnlI   AsuI   MboII   EcoRI   HhaII
```

FIG. 30

1120 1140 1160 1180 1200

HISPHESERCYSLEULYSASPARGHISASPPHEGLYPHEPROGLUGLUGLUPHEASPGLYHISGLNPHEGLNLYSTHRGLNALAILESERVALLEUHIS

CATTTCTCCTGCCTGAAGGACAGACATGATTTCGGATTCCCCGAGGAGGAGTTTGATGGCCACCAGTTCCAGAAGACTCAAGCCATCTCTGTCCTCCATG

EcoRI MnlI BalI MboIII MnlI

HhaII BspRI HhaI

AvaI

1220 1240 1260 1280 1300

GLUMETILEGLNGLNTHRPHEASNLEUPHESERTHRGLUASPSERSERALAALATRPGLUGLNSERLEULEUGLULYSPHESERTHRGLULEUTYRGLNGLN

AGATGATCCAGCAGACCTTCAATCTCTTCAGCACAGAGGACTCATCTGCTGCTTGGGAACAGAGCCTCCTAGAAAAATTTTCCACTGAACTTTACCAGCA

DpnII EcoRI MboII MnlI BbrsI MnlI EcoRI

HhaII

1320 1340 1360 1380 1400

LEUASNASPLEUGLUALACYSVALILEGLNGLUVALGLYVALGLUGLUTHRPROLEUMETASNVALASPSERILELEUALAVALARGLYSTYRPHEGLN

ACTGAATGACCTGGAAGCATGTGTGATACAGGAGGTTGGGGTGGAAGAGACTCCCCTGATGAATGTGGACTCCATCCTGGCTGTGAGGAAATACTTCCAA

BstnI MnlI MboIIHhaII HhaII BstnI MnlI

1420 1440 1460 1480 1500

ARGILETHRLEUTYRLEUTHRGLULYSLYSTYRSERPROCYSALATRPGLUVALVALARGALAGLUILEMETARGSERLEUSERPHESERTHRASNLEU

AGAATCACTCTTTATCTAACAGAGAAGAAATACAGCCCTTGTGCCTGGGAGGTTGTCAGAGCAGAAATCATGAGATCCCTCTCGTTTTCAACAAACTTGC

HhaII MboII BstnIMnlI EcoRI

DpnII

MnlI

1520 1540 1560 1580 1600

GLNLYSARGLEUARGARGLYSASP

AAAAAAGATTAAGGAGGAAGGATTGAAACCTGGTTCAACATGGAAATGATTCCGACTGACTAATACATTATCTCACACTTTCATGAGTTCTTCCATTTCA

MnlI BstnI HhaII MboII

FIG. 31

```
                 1620                1640                1660                1680                1700
AAGACTCACTTCATAACCACCACGAGTTGAATCAAAATTTTCAAATGTTTTCAGCAGTGTGAAGAAGCTTGGTGTATACCGTGCAGGTACTAGTTCTTTA
  HhaII                     HhaII  EcoRI                    MboII                     RsaI
                                                              BbrI
                                                               AluI

                 1720                1740                1760                1780                1800
CAGATGACAATGCTGATGTCTCTGTTCATCTATTTATTTGAATATTTATTTGTTTTTAAAATTTAAATTATTTTTAATGTGATATCATGAGTACCTTTAC
                                                          EcoRI                          RsaI

                 1820                1840
ATTGTGGTGGATGTAACGATATATGTTCTTCATATTTAGCCAATA
                          MboIII
```

FIG 32